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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=3; day=16; hr=12; min=53; sec=33; ms=701;]

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Application No: 10566851

Version No: 2.0

Input Set:

Output Set:

Started: 2009-02-24 19:38:44.247

Finished: 2009-02-24 19:38:45.863

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 616 ms

Total Warnings: 24

Total Errors: 0

No. of SeqIDs Defined: 38

Actual SeqID Count: 38

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Input Set:

Output Set:

Started: 2009-02-24 19:38:44.247
Finished: 2009-02-24 19:38:45.863
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 616 ms
Total Warnings: 24
Total Errors: 0
No. of SeqIDs Defined: 38
Actual SeqID Count: 38

Error code

Error Description

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Saint-Remy, Jean-Marie

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<141> 2006-02-01

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<151> 2004-08-16

<150> GB 0319118.6

<151> 2003-08-14

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Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe
35 40 45

Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His
50 55 60

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile
65 70 75 80

Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg
85 90 95

Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu
100 105 110

Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala
115 120 125

Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp
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Gly Pro Ser Val Phe
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gtagggccac cgacatcca 240

cacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 300

cctgaagatt ttgcagtgtg ctactgtcag caatatggta cctcagcctt actcactttc 360

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro
65 70 75 80

His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gtagggccac cgacatccca	240
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ggcgggtggcg gatcgcaggt acagctggtg cagtctgggg ctgaggtgaa gaagcctggg	480
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Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser
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Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro
65 70 75 80

His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
100 105 110

Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
115 120 125

Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
145 150 155 160

Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Gln Phe Thr Gly
165 170 175

Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His Trp Val
180 185 190

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro
195 200 205

Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg Val Thr
210 215 220

Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg
225 230 235 240

Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala Asp Asn
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cgactgagga gcctgagatc tgaagatacg gccgtgtatt actgtgtcgg cggtcgagat 360
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Pro Gly Ser Ser Val Met Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
35 40 45

Ser Ser Phe Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Val Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Thr Ala
65 70 75 80

Arg Asn Phe Gln Asn Arg Val Thr Ile Thr Ala Asp Glu Phe Thr Ser
85 90 95

Thr Ala Tyr Ile Arg Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Val Gly Gly Arg Asp Ala Tyr Ser Phe Asp Gly Phe Asp
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